

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/538,000
Source: IFWO
Date Processed by STIC: 11/7/2006

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 11/07/2006

PATENT APPLICATION: US/10/538,000

TIME: 11:46:38

Input Set : N:\Crf4\11032006\K538000.raw

Output Set: N:\CRF4\11072006\J538000.raw

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1 <110> APPLICANT: DSM IP Assets B.V.
2   Pieter J.A.M. PLOMP
3   Lex DE BOER
4   Rutger J. VAN ROOIJEN
5   Roelf B. MEIMA
6 <120> TITLE OF INVENTION: NOVEL FOOD PRODUCTION PROCESS
7 <130> FILE REFERENCE: 4662-25 / 21401USWO
C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/538,000
9 <141> CURRENT FILING DATE: 2005-06-09
10 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/014553
11 <151> PRIOR FILING DATE: 2003-12-18
12 <150> PRIOR APPLICATION NUMBER: EP 02102819.6
13 <151> PRIOR FILING DATE: 2002-12-19
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18 <211> LENGTH: 3223
19 <212> TYPE: DNA
20 <213> ORGANISM: Aspergillus niger
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24   ggctccgaga gttttgatag cagttagccaa ttaactagta gatgctagta ctactctagt      180
25   aatttggggg cgaatgttga atccagctca tgccaattga catctggaga tctccacgag      240
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28   tggggcttat cgtggaagag tcacccccga tatcggtggg ccaagccctt tatcaatcat      420
29   catcctatca gtttccaccc acaagatagc ctatggaccc tgattccctt ctagccacag      480
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32   ttccgaatac acccgccgcc tggcaagcac atgggggtata aaatgctgaa accaggcaag      660
33   atgaattgga agagaagcca gcagagacca tcgcatccgt cttcatcatg cctctcaagc      720
34   cgattctcct gtctgccctg gccagtctcg cctcggcctc tccgctgctc tactcgcgga      780
35   ccaccaatga aaccttcgtc ttcaccaatg ccaatggcct caacttcacc cagatgaaca      840
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37   gtgcgaccga tagttaaccg caactcacag gtggtaccat cgcgggctcc gattccagct      960
38   caaccgccac gaccggctac acctccggag cagtcggggg cctgtccctc atcgatgcgg      1020
39   tgccatccat gctggatgtg gccaatgttg cggcgctcca ggtggccaac gtgggaagcg      1080
40   aggatatcac ctctgacatc ctgatttcca tgtccaagaa gctgaaccgc gttgtatgtg      1140
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42   ccttcttctt ggacgccact gtcaactgtg gcaagccaat tgtcatcgtg ggtgccatgc      1260
43   gcccatccac ggccatctca gctgacgggc ccttcaatct gctcgaagcc gtgacggtgg      1320
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48      tgttttctta tgaggacatg cacaacgaca cctctacaa cgccatctcc agtgggtgcc      1620
49      aggggaattgt ggtgagtgtg atttccttga tctctctcta taaaacttgg aatggacgct      1680
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51      tcgaggatgt catcaaccgt ttggagatcc ctgtcgtgca gagtatgcgc acagtcaatg      1800
52      gggaagtgcc actgtcagac gtgagcagcg acaccgccac ccacatcgcc agtggatacc      1860
53      taaaccggca gaagtccgcg attctgttgg gattgctgct atcccaggga aagaatatca      1920
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55      atataataat gaccggatat tatgatcatg atagattgca atagaaagtg actggatata      2040
56      catcagcaaa ggataccgag ttttgccctc aggcgttcgt agaaaaagtg tatectactg      2100
57      aagatcatga atcatgtctt atcttctggc cccctcgtat ccagggtgtt ggacatgcag      2160
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61      gggactgtct cccgccatta ttctcacaat tcttatcagc acattttccc tgtcgcgctt      2400
62      ggatctgcaa tatttatctt cctcgtcatc acattcccac gaaaagacca tccagacatc      2460
63      ttgctcggta ttctggaccg taagactgtt ttgaaaggca aatgtaaagc gtgattggtc      2520
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72      aaggcttgtc cctggtcaac catcactctg gttattgact agttgtgttt gggagacagc      3060
73      tgaagcccat tgtcggtaat cgtccccaaa gaatctgccc ctgcatcatg gagtccaggaa      3120
74      agaccgggtt tcgcacggtc gcagaaccgc atccaacacg tctagtagaa ggaggggtag      3180
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83 <222> LOCATION: (1)..(1137)
84 <400> SEQUENCE: 2
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86      Met Pro Leu Lys Pro Ile Leu Leu Ser Ala Leu Ala Ser Leu Ala Ser
87      1          5          10          15
88      gcc tct ccg ctg ctc tac tcg cgg acc acc aat gaa acc ttc gtc ttc      96
89      Ala Ser Pro Leu Leu Tyr Ser Arg Thr Thr Asn Glu Thr Phe Val Phe
90      20          25          30
91      acc aat gcc aat ggc ctc aac ttc acc cag atg aac acc acc ctg ccg      144
92      Thr Asn Ala Asn Gly Leu Asn Phe Thr Gln Met Asn Thr Thr Leu Pro
93      35          40          45
94      aac gtg acc att ttc gca acg ggt ggt acc atc gcg ggc tcc gat tcc      192

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97	agc tca acc gcc acg acc ggc tac acc tcc gga gca gtc ggg gtc ctg	240
98	Ser Ser Thr Ala Thr Thr Gly Tyr Thr Ser Gly Ala Val Gly Val Leu	
99	65 70 75 80	
100	tcc ctc atc gat gcg gtg cca tcc atg ctg gat gtg gcc aat gtt gcc	288
101	Ser Leu Ile Asp Ala Val Pro Ser Met Leu Asp Val Ala Asn Val Ala	
102	85 90 95	
103	ggc gtc cag gtg gcc aac gtg gga agc gag gat atc acc tct gac atc	336
104	Gly Val Gln Val Ala Asn Val Gly Ser Glu Asp Ile Thr Ser Asp Ile	
105	100 105 110	
106	ctg att tcc atg tcc aag aag ctg aac cgc gtt gta tgt gag gac ccg	384
107	Leu Ile Ser Met Ser Lys Lys Leu Asn Arg Val Val Cys Glu Asp Pro	
108	115 120 125	
109	acc atg gcc ggt gct gtc atc acc cac ggc acc gac acc ctc gag gag	432
110	Thr Met Ala Gly Ala Val Ile Thr His Gly Thr Asp Thr Leu Glu Glu	
111	130 135 140	
112	act gcc ttc ttc ctg gac gcc act gtc aac tgt ggc aag cca att gtc	480
113	Thr Ala Phe Phe Leu Asp Ala Thr Val Asn Cys Gly Lys Pro Ile Val	
114	145 150 155 160	
115	atc gtg ggt gcc atg cgc cca tcc acg gcc atc tca gct gac ggg ccc	528
116	Ile Val Gly Ala Met Arg Pro Ser Thr Ala Ile Ser Ala Asp Gly Pro	
117	165 170 175	
118	ttc aat ctg ctc gaa gcc gtg acg gtg gct gcc tcc acg tcc ggc cgc	576
119	Phe Asn Leu Leu Glu Ala Val Thr Val Ala Ala Ser Thr Ser Ala Arg	
120	180 185 190	
121	gat cgc ggt gcc atg gtg gtc atg aac gat cgc att gcc tcc gcc tac	624
122	Asp Arg Gly Ala Met Val Val Met Asn Asp Arg Ile Ala Ser Ala Tyr	
123	195 200 205	
124	tat gtg acc aag acc aat gcc aac act atg gac acc ttc aag gcc atg	672
125	Tyr Val Thr Lys Thr Asn Ala Asn Thr Met Asp Thr Phe Lys Ala Met	
126	210 215 220	
127	gag atg ggc tac ctt ggc gag atg atc tcc aac acc cct ttc ttc ttc	720
128	Glu Met Gly Tyr Leu Gly Glu Met Ile Ser Asn Thr Pro Phe Phe Phe	
129	225 230 235 240	
130	tac ccg ccc gtc aag cca acc ggt aag gtg gcc ttt gac atc acc aac	768
131	Tyr Pro Pro Val Lys Pro Thr Gly Lys Val Ala Phe Asp Ile Thr Asn	
132	245 250 255	
133	gtg act gag atc ccc cgt gtg gac att ctg ttt tct tat gag gac atg	816
134	Val Thr Glu Ile Pro Arg Val Asp Ile Leu Phe Ser Tyr Glu Asp Met	
135	260 265 270	
136	cac aac gac acc ctc tac aac gcc atc tcc agt ggt gcc cag gga att	864
137	His Asn Asp Thr Leu Tyr Asn Ala Ile Ser Ser Gly Ala Gln Gly Ile	
138	275 280 285	
139	gtg att gcc ggg gct ggt gct gga ggc gtc aca acc tcc ttc aat gag	912
140	Val Ile Ala Gly Ala Gly Ala Gly Gly Val Thr Ser Phe Asn Glu	
141	290 295 300	
142	gct atc gag gat gtc atc aac cgt ttg gag atc cct gtc gtg cag agt	960
143	Ala Ile Glu Asp Val Ile Asn Arg Leu Glu Ile Pro Val Val Gln Ser	

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145      atg cgc aca gtc aat ggg gaa gtg cca ctg tca gac gtg agc agc gac      1008
146      Met Arg Thr Val Asn Gly Glu Val Pro Leu Ser Asp Val Ser Ser Asp
147      325      330      335
148      acc gcc acc cac atc gcc agt gga tac cta aac ccg cag aag tcc cgc      1056
149      Thr Ala Thr His Ile Ala Ser Gly Tyr Leu Asn Pro Gln Lys Ser Arg
150      340      345      350
151      att ctg ttg gga ttg ctg cta tcc cag gga aag aat atc acc gaa atc      1104
152      Ile Leu Leu Gly Leu Leu Leu Ser Gln Gly Lys Asn Ile Thr Glu Ile
153      355      360      365
154      gct gac gtg ttt gct ctg ggc acg gat gcg tag      1137
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156      370      375
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159 <211> LENGTH: 378
160 <212> TYPE: PRT
161 <213> ORGANISM: Aspergillus niger
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165      Ala Ser Pro Leu Leu Tyr Ser Arg Thr Thr Asn Glu Thr Phe Val Phe
166      20      25      30
167      Thr Asn Ala Asn Gly Leu Asn Phe Thr Gln Met Asn Thr Thr Leu Pro
168      35      40      45
169      Asn Val Thr Ile Phe Ala Thr Gly Gly Thr Ile Ala Gly Ser Asp Ser
170      50      55      60
171      Ser Ser Thr Ala Thr Thr Gly Tyr Thr Ser Gly Ala Val Gly Val Leu
172      65      70      75      80
173      Ser Leu Ile Asp Ala Val Pro Ser Met Leu Asp Val Ala Asn Val Ala
174      85      90      95
175      Gly Val Gln Val Ala Asn Val Gly Ser Glu Asp Ile Thr Ser Asp Ile
176      100      105      110
177      Leu Ile Ser Met Ser Lys Lys Leu Asn Arg Val Val Cys Glu Asp Pro
178      115      120      125
179      Thr Met Ala Gly Ala Val Ile Thr His Gly Thr Asp Thr Leu Glu Glu
180      130      135      140
181      Thr Ala Phe Phe Leu Asp Ala Thr Val Asn Cys Gly Lys Pro Ile Val
182      145      150      155      160
183      Ile Val Gly Ala Met Arg Pro Ser Thr Ala Ile Ser Ala Asp Gly Pro
184      165      170      175
185      Phe Asn Leu Leu Glu Ala Val Thr Val Ala Ala Ser Thr Ser Ala Arg
186      180      185      190
187      Asp Arg Gly Ala Met Val Val Met Asn Asp Arg Ile Ala Ser Ala Tyr
188      195      200      205
189      Tyr Val Thr Lys Thr Asn Ala Asn Thr Met Asp Thr Phe Lys Ala Met
190      210      215      220
191      Glu Met Gly Tyr Leu Gly Glu Met Ile Ser Asn Thr Pro Phe Phe Phe
192      225      230      235      240
193      Tyr Pro Pro Val Lys Pro Thr Gly Lys Val Ala Phe Asp Ile Thr Asn

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194		245		250		255
195	Val Thr Glu Ile Pro Arg Val Asp Ile Leu Phe Ser Tyr Glu Asp Met					
196		260		265		270
197	His Asn Asp Thr Leu Tyr Asn Ala Ile Ser Ser Gly Ala Gln Gly Ile					
198		275		280		285
199	Val Ile Ala Gly Ala Gly Ala Gly Gly Val Thr Thr Ser Phe Asn Glu					
200		290		295		300
201	Ala Ile Glu Asp Val Ile Asn Arg Leu Glu Ile Pro Val Val Gln Ser					
202		305		310		315
203	Met Arg Thr Val Asn Gly Glu Val Pro Leu Ser Asp Val Ser Ser Asp					
204		325		330		335
205	Thr Ala Thr His Ile Ala Ser Gly Tyr Leu Asn Pro Gln Lys Ser Arg					
206		340		345		350
207	Ile Leu Leu Gly Leu Leu Leu Ser Gln Gly Lys Asn Ile Thr Glu Ile					
208		355		360		365
209	Ala Asp Val Phe Ala Leu Gly Thr Asp Ala					
210		370		375		

RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : N:\Crf4\11032006\K538000.raw

Output Set: N:\CRF4\11072006\J538000.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57

Seq#:1; Line(s) 58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75

Seq#:2; Line(s) 145,148,151,154

VERIFICATION SUMMARY

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Input Set : N:\Crf4\11032006\K538000.raw

Output Set: N:\CRF4\11072006\J538000.raw

L:8 M:270 C: Current Application Number differs, Replaced Current Application Number